

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 10:13:23 ; Search time 346.117 Seconds
(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-1

Perfect score: 18

Sequence: 1 cgcaagctgaaaaagtag 18

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 9794790 seqs, 413490567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*

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28: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	18	100.0	24	16 US-10-025-137-3	Sequence 3, Appli
C 3	16.4	91.1	233	21 US-10-425-115-157137	Sequence 157137,
4	16.4	91.1	700	14 US-10-027-632-149388	Sequence 149388,
5	16.4	91.1	700	18 US-10-027-632-149388	Sequence 149388,

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6 16.4 91.1 2310 18 US-10-369-493-46035 Sequence 46035, A
7 16.4 91.1 2490 9 US-09-974-300-4328 Sequence 4328, Ap
8 16.4 91.1 3490 24 US-10-510-408-48 Sequence 48, Appl
9 16 88.9 351 20 US-10-430-201-2755 Sequence 2755, Ap
10 16 88.9 351 20 US-10-430-201-2756 Sequence 2756, Ap
11 16 88.9 1592 21 US-10-723-860-2804 Sequence 2804, Ap
12 16 88.9 1834 21 US-10-723-860-6882 Sequence 6882, Ap
13 16 88.9 2940 10 US-09-814-353-21490 Sequence 21490, A
14 15.4 85.6 393 22 US-10-472-928-11003 Sequence 11003, Ap
15 15.4 85.6 488 10 US-09-770-961-739 Sequence 739, App
16 15.4 85.6 493 13 US-09-925-065A-747566 Sequence 747566,
17 15.4 85.6 493 13 US-09-925-065A-747567 Sequence 747567,
18 15.4 85.6 493 13 US-09-925-065A-747568 Sequence 747568,
19 15.4 85.6 555 18 US-10-282-122A-27952 Sequence 27952, A
20 15.4 85.6 589 13 US-09-925-065A-619093 Sequence 619093,
21 15.4 85.6 612 13 US-09-925-065A-731537 Sequence 731537,
22 15.4 85.6 612 13 US-09-925-065A-731538 Sequence 731538,
23 15.4 85.6 653 13 US-09-925-065A-274420 Sequence 274420,
24 15.4 85.6 653 13 US-09-925-065A-274421 Sequence 274421,
25 15.4 85.6 653 13 US-09-925-065A-274422 Sequence 274422,
26 15.4 85.6 963 19 US-10-424-599-50975 Sequence 50975, A
27 15.4 85.6 1200 21 US-10-739-930-3873 Sequence 3873, Ap
28 15.4 85.6 1221 18 US-10-369-493-43501 Sequence 43501, A
29 15.4 85.6 1260 13 US-09-925-065A-674296 Sequence 674296,
30 15.4 85.6 1503 9 US-09-974-300-481 Sequence 481, App
31 15.4 85.6 1539 9 US-09-974-300-493 Sequence 493, App
32 15.4 85.6 2658 18 US-10-282-122A-26897 Sequence 26897, A
33 15.4 85.6 11378 8 US-08-961-527-210 Sequence 210, App
34 15.4 85.6 11378 18 US-10-158-844-210 Sequence 210, App
35 15.4 85.6 92407 19 US-10-672-787-36 Sequence 36, Appl
36 15.4 85.6 203264 14 US-10-087-192-988 Sequence 988, App
37 15.4 85.6 253861 20 US-10-741-601-5611 Sequence 5611, Ap
38 15.4 85.6 261817 14 US-10-087-192-2002 Sequence 2002, Ap
39 15.4 85.6 385320 22 US-10-741-600-17796 Sequence 17796, A
40 15.4 85.6 2162598 22 US-10-472-928-4979 Sequence 4979, Ap
41 15 83.3 25 22 US-10-719-900-310367 Sequence 310367,
42 15 83.3 25 22 US-10-719-900-364148 Sequence 364148,
43 15 83.3 25 22 US-10-719-900-560295 Sequence 560295,
44 15 83.3 25 22 US-10-719-900-610415 Sequence 610415,
45 15 83.3 25 22 US-10-719-900-618457 Sequence 618457,
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ALIGNMENTS

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RESULT 1
US-10-025-137-1
; Sequence 1, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Terng, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-085001
; CURRENT APPLICATION NUMBER: US/10/025,137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated primer
US-10-025-137-1
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Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAAGCTGAAAAAGTAG 18
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 06:12:54 ; Search time 46.7435 Seconds
(without alignments)
630.098 Million cell updates/sec

Title: US-10-025-137B-1

Perfect score: 18
Sequence: 1 CGCAAGCTGAAAAGTAG 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgm2_6/ptodata/1/ina/5A_COMB.seq:
2: /cgm2_6/ptodata/1/ina/5B_COMB.seq:
3: /cgm2_6/ptodata/1/ina/6A_COMB.seq:
4: /cgm2_6/ptodata/1/ina/6B_COMB.seq:
5: /cgm2_6/ptodata/1/ina/PCTUS_COMB.seq:
6: /cgm2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 2	16.4	91.1	24280	4	US-09-949-016-15622
C 3	15.4	85.6	396	4	US-09-583-110-234
4	15.4	85.6	601	4	US-09-949-016-76457
5	15.4	85.6	601	4	US-09-949-016-76458
6	15.4	85.6	999	4	US-09-902-540-8492
7	15.4	85.6	1914	4	US-09-540-236-1278
8	15.4	85.6	2256	4	US-09-540-236-400
9	15.4	85.6	7538	4	US-09-902-540-894
10	15.4	85.6	11378	3	US-08-961-527-210
C 11	15.4	85.6	31861	4	US-09-949-016-12803
C 12	15.4	85.6	31861	4	US-09-949-016-13967
13	15.4	85.6	92407	4	US-09-586-002-36
14	15.4	85.6	141248	4	US-09-949-016-12241
15	15.4	85.6	143248	4	US-09-949-016-16652
16	15.4	85.6	194937	4	US-09-949-016-17032
17	15.4	85.6	194937	4	US-09-949-016-17033
18	15.4	85.6	200663	4	US-09-949-016-12569
19	15.4	85.6	203093	4	US-09-949-016-14445
20	15.4	85.6	818128	4	US-09-949-016-14547
21	15.4	85.6	818128	4	US-09-949-016-14547
22	15.4	85.6	818128	4	US-09-949-016-14547
23	15.4	85.6	818128	4	US-09-949-016-14549
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25	15.4	85.6	818128	4	US-09-949-016-14551
26	15.4	85.6	818128	4	US-09-949-016-14552
27	15.4	85.6	818128	4	US-09-949-016-14553

28	15.4	85.6	818128	4	US-09-949-016-14554	Sequence 14554, A
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33	15.4	85.6	818128	4	US-09-949-016-14559	Sequence 14559, A
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35	15.4	85.6	818128	4	US-09-949-016-14561	Sequence 14561, A
36	15.4	85.6	818128	4	US-09-949-016-14562	Sequence 14562, A
37	15.4	85.6	818128	4	US-09-949-016-14563	Sequence 14563, A
38	15.4	85.6	818128	4	US-09-949-016-14564	Sequence 14564, A
39	15.4	85.6	818128	4	US-09-949-016-14565	Sequence 14565, A
40	15.4	85.6	818128	4	US-09-949-016-14566	Sequence 14566, A
C 41	15	83.3	601	4	US-09-949-016-38946	Sequence 38946, A
C 42	15	83.3	601	4	US-09-949-016-38947	Sequence 38947, A
C 43	15	83.3	601	4	US-09-949-016-38948	Sequence 38948, A
C 44	15	83.3	601	4	US-09-949-016-38949	Sequence 38949, A
45	15	83.3	601	4	US-09-949-016-128437	Sequence 128437, A

ALIGNMENTS

RESULT 1
US-09-949-016-15621/c
; Sequence 15621, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15621
; LENGTH: 24280
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15621

Query Match 91.1%; Score 16.4; DB 4; Length 24280;
Best Local Similarity 94.4%; Pred. No. 1.5e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CGCAAGCTGAAAAGTAG 18
DB 18059 CGCAAGCTGAAAAGTAG 18042

RESULT 2
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; Sequence 15622, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 10:13:23 ; Search time 499.99 Seconds
(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-8

Perfect score: 26

Sequence: 1 gttatgtattgctgttgcggcg 26

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
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24: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
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28: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	18.8	72.3	765	20	Sequence 8, Appl1
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4	18.8	72.3	914	18	Sequence 325205,
5	18.6	71.5	507	19	Sequence 325205,
					Sequence 106771,

c 6	18.6	71.5	516	13	US-09-925-065A-284063	Sequence 284063,
c 7	18.6	71.5	516	13	US-09-925-065A-284064	Sequence 284064,
c 8	18.6	71.5	538	13	US-09-925-065A-586080	Sequence 586080,
9	18.6	71.5	538	13	US-09-925-065A-586081	Sequence 586081,
10	18.6	71.5	538	13	US-09-925-065A-586082	Sequence 586082,
11	18.6	71.5	591	13	US-09-925-065A-636500	Sequence 636500,
c 12	18.6	71.5	612	13	US-09-925-065A-377540	Sequence 377540,
c 13	18.6	71.5	612	13	US-09-925-065A-377541	Sequence 377541,
c 14	18.6	71.5	612	13	US-09-925-065A-377542	Sequence 377542,
c 15	18.6	71.5	612	13	US-09-925-065A-377543	Sequence 377543,
16	18.6	71.5	620	13	US-09-925-065A-414588	Sequence 414588,
17	18.6	71.5	620	13	US-09-925-065A-414589	Sequence 414589,
18	18.6	71.5	620	13	US-09-925-065A-414590	Sequence 414590,
19	18.6	71.5	1112	26	US-10-424-599-106760	Sequence 106760,
c 20	18.6	71.5	3156	19	US-11-097-143-8716	Sequence 8716, Ap
c 21	18.6	71.5	4331	26	US-11-097-143-8716	Sequence 8716, Ap
c 22	18.6	71.5	6426	26	US-11-097-143-8716	Sequence 8716, Ap
23	18.4	70.8	846	9	US-09-801-368-277	Sequence 277, App
24	18.4	70.8	846	18	US-10-369-493-25289	Sequence 25289, A
c 25	18.2	70.0	454	13	US-09-925-065A-96568	Sequence 96568, A
c 26	18.2	70.0	454	13	US-09-925-065A-96569	Sequence 96569, A
c 27	18.2	70.0	544	20	US-10-021-323-16363	Sequence 16363, A
c 28	18.2	70.0	553	13	US-09-925-065A-123177	Sequence 123177,
c 29	18.2	70.0	553	13	US-09-925-065A-123178	Sequence 123178,
c 30	18.2	70.0	553	13	US-09-925-065A-220655	Sequence 220655,
c 31	18.2	70.0	553	13	US-09-925-065A-220656	Sequence 220656,
32	18.2	70.0	581	13	US-09-925-065A-872784	Sequence 872784,
33	18.2	70.0	590	20	US-10-021-323-14869	Sequence 14869, A
34	18.2	70.0	617	9	US-09-974-300-1766	Sequence 1766, Ap
35	18.2	70.0	666	13	US-09-925-065A-677902	Sequence 677902,
36	18.2	70.0	814	20	US-10-767-795-5675	Sequence 5675, Ap
37	18.2	70.0	1011	18	US-10-369-493-35117	Sequence 35117, A
38	18.2	70.0	1011	18	US-10-369-493-38288	Sequence 38288, A
39	18.2	70.0	1011	18	US-10-369-493-38680	Sequence 38680, A
c 40	18.2	70.0	640681	9	US-09-790-988-1	Sequence 1, Appli
c 41	18	69.2	403	20	US-10-437-963-59536	Sequence 59536, A
c 42	18	69.2	600	24	US-10-972-079-48473	Sequence 48473, A
c 43	18	69.2	600	24	US-10-972-079-48474	Sequence 48474, A
c 44	18	69.2	612	13	US-09-925-065A-269722	Sequence 269722,
45	18	69.2	1075	13	US-09-925-065A-727798	Sequence 727798,

ALIGNMENTS

RESULT 1
US-10-025-137-8
; Sequence 8, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Terng, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025,137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated probe
US-10-025-137-8

Query Match 100.0%; Score 26; DB 16; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTTATGTTGCTGCTGTTGCGGCG 26
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 10:13:23 ; Search time 519.22 Seconds
(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-7

Perfect score: 27
Sequence: 1 attttaccttctgtctcccgctttgg 27

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US11_PUBCOMB.seq.*
- 27: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 28: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	27	100.0	4402	24	US-10-450-763-25521
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4	20.6	76.3	599	13	US-09-925-065A-745980
5	19.8	73.3	445	13	US-09-925-065A-290213

6	19.6	72.6	600	24	US-10-972-079-31542	Sequence 31542, A
7	19.6	72.6	600	24	US-10-972-079-31543	Sequence 31543, A
8	19.6	72.6	600	24	US-10-972-079-31544	Sequence 31544, A
9	19.6	72.6	600	24	US-10-972-079-31545	Sequence 31545, A
10	19.6	72.6	676	19	US-10-425-114-31270	Sequence 31270, A
11	19.6	72.6	676	21	US-10-425-115-134950	Sequence 134950, A
12	19.6	72.6	722	9	US-09-966-881-8	Sequence 8, Appli
13	19.6	72.6	730	19	US-10-425-114-5874	Sequence 5874, Ap
14	19.6	72.6	1293	19	US-10-425-114-31738	Sequence 31738, A
15	19.6	72.6	1318	21	US-10-425-115-134956	Sequence 134956, A
16	19.6	72.6	1334	21	US-10-425-115-134954	Sequence 134954, A
17	19.6	72.6	1460	19	US-10-425-114-34241	Sequence 34241, A
18	19.6	72.6	1460	21	US-10-425-115-134948	Sequence 134948, A
19	19	70.4	368	18	US-10-242-535A-40004	Sequence 40004, A
20	19	70.4	368	19	US-10-085-783A-40004	Sequence 40004, A
21	19	70.4	594	13	US-09-925-065A-932387	Sequence 932387, A
22	19	70.4	600	13	US-09-925-065A-233255	Sequence 233255, A
23	19	70.4	600	13	US-09-925-065A-233256	Sequence 233256, A
24	19	70.4	600	13	US-09-925-065A-233257	Sequence 233257, A
25	19	70.4	600	24	US-10-972-079-24595	Sequence 24595, A
26	19	70.4	1112	13	US-09-925-065A-283732	Sequence 283732, A
27	19	70.4	7372	24	US-10-073-735A-1	Sequence 1, Appli
28	18.6	68.9	453	13	US-09-925-065A-561153	Sequence 561153, A
29	18.6	68.9	482	14	US-10-027-632-188723	Sequence 188723, A
30	18.6	68.9	482	14	US-10-027-632-188724	Sequence 188724, A
31	18.6	68.9	482	18	US-10-027-632-188723	Sequence 188723, A
32	18.6	68.9	482	18	US-10-027-632-188724	Sequence 188724, A
33	18.6	68.9	573	13	US-09-925-065A-453195	Sequence 453195, A
34	18.6	68.9	589	13	US-09-925-065A-742966	Sequence 742966, A
35	18.6	68.9	589	13	US-09-925-065A-818062	Sequence 818062, A
36	18.6	68.9	624	13	US-09-925-065A-838563	Sequence 838563, A
37	18.6	68.9	624	13	US-09-925-065A-838564	Sequence 838564, A
38	18.6	68.9	657	13	US-09-925-065A-514497	Sequence 514497, A
39	18.6	68.9	1754	26	US-11-097-143-25148	Sequence 25148, A
40	18.6	68.9	2275	13	US-09-925-065A-686407	Sequence 686407, A
41	18.6	68.9	2275	13	US-09-925-065A-686408	Sequence 686408, A
42	18.6	68.9	2275	13	US-09-925-065A-686409	Sequence 686409, A
43	18.6	68.9	2275	13	US-09-925-065A-686410	Sequence 686410, A
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45	18.6	68.9	2275	13	US-09-925-065A-686412	Sequence 686412, A

ALIGNMENTS

RESULT 1
US-10-025-137-7
; Sequence 7: Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Tereng, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025,137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated probe
US-10-025-137-7

Query Match 100.0%; Score 27; DB 16; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATTTTACCTTGTCTTCCCGCTTTGG 27
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 10:13:23 ; Search time 519.22 Seconds
(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-6
Perfect score: 27
Sequence: 1 aaacacctctctcgattctcac 27

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues
Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :				Published Applications NA:*	
1:	/cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:				
2:	/cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:				
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5:	/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:				
6:	/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:				
7:	/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:				
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22:	/cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq:				
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28:	/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:				

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	16	US-10-025-137-6
C 2	21.2	78.5	585	19	US-10-424-599-82584
C 3	19.8	73.3	731	24	US-10-450-763-21628
4	19.8	73.3	2681	19	US-10-467-042-26
5	19.8	73.3	2681	26	US-11-046-868-26

C 6	19.6	72.6	329	21	US-10-856-498-1702
C 7	19.6	72.6	348	21	US-10-856-499-1742
C 8	19.6	72.6	449	10	US-09-918-995-15975
C 9	19.2	71.1	6888	21	US-10-602-494-20
C 10	19.2	71.1	6888	21	US-10-602-494-110
C 11	19	70.4	1204	17	US-10-029-386-22637
C 12	19	70.4	2602	9	US-09-974-298-45
C 13	19	70.4	9012	24	US-10-450-763-3921
C 14	19	70.4	9012	24	US-10-450-763-8552
C 15	19	70.4	9633	22	US-10-956-157-4420
C 16	19	70.4	10184	24	US-10-450-763-23875
C 17	18.8	69.6	33805	14	US-10-087-192-1483
C 18	18.6	68.9	201	21	US-10-719-993-19568
C 19	18.6	68.9	201	22	US-10-741-600-39403
C 20	18.6	68.9	580	13	US-09-925-065A-571437
C 21	18.6	68.9	626	13	US-09-925-065A-483342
C 22	18.6	68.9	672	14	US-10-767-701-8672
C 23	18.6	68.9	672	14	US-10-027-632-206505
C 24	18.6	68.9	840	18	US-10-282-122A-10840
C 25	18.6	68.9	1506	26	US-11-097-143-37523
C 26	18.6	68.9	1908	18	US-10-369-493-33615
C 27	18.6	68.9	2681	24	US-10-765-700-108
C 28	18.6	68.9	3528	9	US-09-350-259-36
C 29	18.6	68.9	3528	10	US-09-891-943-36
C 30	18.6	68.9	3597	9	US-09-350-259-54
C 31	18.6	68.9	3597	10	US-09-891-943-54
C 32	18.6	68.9	3742	26	US-11-097-143-37522
C 33	18.6	68.9	5806	26	US-11-097-143-42871
C 34	18.6	68.9	1980090	21	US-10-719-993-6815
C 35	18.6	68.9	1980090	22	US-10-741-600-17676
C 36	18.4	68.1	587	13	US-09-925-065A-96162
C 37	18.4	68.1	587	13	US-09-925-065A-96163
C 38	18.4	68.1	518	20	US-10-437-963-83395
C 39	18.4	67.4	666	20	US-10-437-963-9460
C 40	18.2	67.4	681	13	US-09-925-065A-706860
C 41	18.2	67.4	681	13	US-09-925-065A-706861
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C 45	18.2	67.4			

ALIGNMENTS

RESULT 1
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; Sequence 6, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025.137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated probe
US-10-025-137-6

Query Match 100.0%; Score 27; DB 16; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.019; 0; Gaps 0;
Matches 27; Conservative 0; Mismatches 0; Indels 0;

1 AAACACCTCTCTCGGATTCTCAC 27
|||||

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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 06:12:54 ; Search time 70.1152 Seconds
(without alignments)
630.098 Million cell updates/sec

Title: US-10-025-137B-6

Perfect score: 27
Sequence: 1 aaacacctctctctgagattcttcac 27

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	19.6	72.6	329	4	US-09-640-211A-1702
C 2	19.6	72.6	348	4	US-09-640-211A-1742
C 3	19.2	71.1	601	4	US-09-949-016-65388
C 4	19.2	71.1	45225	4	US-09-949-016-12428
C 5	19.2	71.1	45226	4	US-09-949-016-13654
C 6	19	70.4	1509	4	US-09-252-991A-5586
C 7	19	70.4	1524	4	US-09-252-991A-5643
C 8	18.6	68.9	2681	4	US-09-566-921-108
C 9	18.6	68.9	3528	1	US-08-286-889-36
C 10	18.6	68.9	3528	1	US-08-485-618-36
C 11	18.6	68.9	3528	1	US-08-362-652-36
C 12	18.6	68.9	3528	1	US-08-605-672-36
C 13	18.6	68.9	3528	2	US-08-482-293A-36
C 14	18.6	68.9	3528	2	US-08-943-363-36
C 15	18.6	68.9	3528	3	US-09-193-043-36
C 16	18.6	68.9	3528	3	US-09-688-307A-36
C 17	18.6	68.9	3528	4	US-09-350-259-36
C 18	18.6	68.9	3597	1	US-08-485-618-54
C 19	18.6	68.9	3597	1	US-08-362-652-54
C 20	18.6	68.9	3597	1	US-08-605-672-54
C 21	18.6	68.9	3597	2	US-08-482-293A-54
C 22	18.6	68.9	3597	2	US-08-943-363-54
C 23	18.6	68.9	3597	3	US-09-193-043-54
C 24	18.6	68.9	3597	3	US-09-688-307A-54
C 25	18.6	68.9	3597	4	US-09-350-259-54
C 26	18	66.7	1766	4	US-09-167-206-11
C 27	18	66.7	1845	4	US-09-949-016-1779

C	28	18	66.7	1851	4	US-09-949-016-480	Sequence 480, App
	29	18	66.7	78649	4	US-09-949-016-14619	Sequence 14619, A
	30	18	66.7	78649	4	US-09-949-016-14620	Sequence 14620, A
	31	18	66.7	78649	4	US-09-949-016-16227	Sequence 16227, A
	32	18	66.7	78649	4	US-09-949-016-16228	Sequence 16228, A
	33	18	66.7	83665	4	US-09-949-016-16995	Sequence 16995, A
C	34	18	66.7	221958	4	US-09-949-016-12173	Sequence 12173, A
	35	18	66.7	221966	4	US-09-949-016-15498	Sequence 15498, A
	36	17.6	65.2	601	4	US-09-949-016-38523	Sequence 38523, A
	37	17.6	65.2	601	4	US-09-949-016-152047	Sequence 152047, A
	38	17.6	65.2	601	4	US-09-949-016-152120	Sequence 152120, A
	39	17.6	65.2	601	4	US-09-949-016-152193	Sequence 152193, A
	40	17.6	65.2	601	4	US-09-949-016-152266	Sequence 152266, A
	41	17.6	65.2	601	4	US-09-949-016-159352	Sequence 159352, A
	42	17.6	65.2	601	4	US-09-949-016-159425	Sequence 159425, A
	43	17.6	65.2	601	4	US-09-949-016-159498	Sequence 159498, A
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ALIGNMENTS

RESULT 1
US-09-640-211A-1702/c
; Sequence 1702, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640.211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1702
; LENGTH: 329
; TYPE: DNA
; ORGANISM: Pinus radiata
US-09-640-211A-1702

Query Match 72.6%; Score 19.6; DB 4; Length 329;
Best Local Similarity 84.6%; Pred No. 17;
Matches 22; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Db 234 AAACACCTCTCTCTGCTTCTCTCA 209

RESULT 2
US-09-640-211A-1742/c
; Sequence 1742, Application US/09640211A
; Patent No. 6833446
; GENERAL INFORMATION:
; APPLICANT: Wood, Marion
; APPLICANT: Shenk, Michael A.
; APPLICANT: McGrath, Annette
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1021CIU
; CURRENT APPLICATION NUMBER: US/09/640.211A
; CURRENT FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 2368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1742
; LENGTH: 348
; TYPE: DNA

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 10:13:23 ; Search time 519.22 Seconds
(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-5

Perfect score: 27

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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA.*
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3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
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14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
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17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
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20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
22: /cgn2_6/ptodata/2/pubpna/US10J_PUBCOMB.seq.*
23: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
24: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
25: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
26: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
27: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*
28: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	100.0	27	16	US-10-025-137-5
C 2	21.2	78.5	731	18	Sequence 5, Appli
C 3	20.6	76.3	572	13	Sequence 472, App
C 4	20.6	76.3	572	13	Sequence 197203,
C 5	20.2	74.8	266	13	Sequence 197204,
					Sequence 18595, A

6	20.2	74.8	550	13	US-09-925-065A-532578	Sequence 532578,
7	20.2	74.8	580	13	US-09-925-065A-374894	Sequence 374894,
8	20.2	74.8	616	13	US-09-925-065A-532579	Sequence 532579,
9	20.2	74.8	637	10	US-09-925-065A-532579	Sequence 58, Appl
C 10	20.2	74.8	637	13	US-09-925-065A-445185	Sequence 445185,
C 11	20.2	74.8	643	13	US-09-925-065A-445186	Sequence 445186,
C 12	20.2	74.8	643	13	US-09-925-065A-445187	Sequence 445187,
C 13	20.2	74.8	830	14	US-10-027-632-174075	Sequence 174075,
C 14	20.2	74.8	830	18	US-10-027-632-174075	Sequence 174075,
C 15	20.2	74.8	119472	22	US-10-741-600-17865	Sequence 17865, A
C 16	20.2	74.8	235015	22	US-10-741-600-17611	Sequence 17611, A
C 17	20.2	74.8	854	19	US-10-425-114-953	Sequence 953, App
C 18	20.2	74.8	919	21	US-10-425-115-30589	Sequence 30589, A
C 19	20.2	74.8	1282	21	US-10-739-330-172	Sequence 172, App
C 20	20.2	74.8	6565	19	US-10-221-714A-187	Sequence 187, App
C 21	20.2	74.8	7002	9	US-09-954-456-1247	Sequence 1247, App
C 22	20.2	74.8	7002	22	US-10-843-641A-4274	Sequence 4274, App
C 23	20.2	74.8	96592	11	US-09-997-722-88	Sequence 88, Appl
C 24	20.2	74.8	163350	22	US-10-469-052-3	Sequence 3, Appl
C 25	20.2	74.8	167343	9	US-09-962-436-281	Sequence 281, App
C 26	20.2	74.8	167343	9	US-09-964-824A-273	Sequence 273, App
C 27	20.2	74.8	167343	22	US-10-843-641A-2740	Sequence 2740, App
C 28	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 29	20.2	74.8	167343	22	US-10-242-535A-46244	Sequence 46244, A
C 30	20.2	74.8	167343	22	US-10-085-783A-46244	Sequence 46244, A
C 31	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 32	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 33	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 34	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 35	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 36	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 37	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 38	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 39	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 40	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 41	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 42	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 43	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 44	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App
C 45	20.2	74.8	167343	22	US-10-843-641A-5576	Sequence 5576, App

ALIGNMENTS

RESULT 1
US-10-025-137-5
; Sequence 5, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Teng, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025.137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated probe
US-10-025-137-5

Query Match 100.0%; Score 27; DB 16; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATACATACAGAACTGAACACAA 27
|||||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 06:12:54 ; Search time 70.1152 Seconds
(without alignments)
630.098 Million cell updates/sec

Title: US-10-025-137B-5

Perfect score: 27

Sequence: 1 aatacataacagaacctgaacacaa 27

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	19.2	71.1	25190	4	US-09-949-016-15906
3	19.2	71.1	69263	4	US-09-949-016-12594
4	19.2	71.1	69709	4	US-09-949-016-16036
5	19.2	71.1	194915	4	US-09-949-016-15584
6	19	70.4	587	4	US-09-270-767-11712
7	19	70.4	601	4	US-09-949-016-147450
8	19	70.4	601	4	US-09-949-016-147451
9	19	70.4	77388	4	US-09-949-016-13496
10	19	70.4	78491	4	US-09-949-016-15132
11	19	70.4	87470	4	US-09-949-016-15881
12	19	70.4	107085	4	US-09-949-016-13157
13	19	70.4	115388	4	US-09-949-016-14981
14	19	70.4	127771	4	US-09-949-016-14982
15	19	70.4	253345	4	US-09-949-016-12656
16	19	70.4	253364	4	US-09-949-016-13639
17	18.6	68.9	112623	4	US-09-949-016-14374
18	18.2	67.4	1013	4	US-09-270-767-11613
19	18	66.7	451	4	US-09-679-409-49
20	18	66.7	601	4	US-09-949-016-69420
21	18	66.7	601	4	US-09-949-016-127473
22	18	66.7	601	4	US-09-949-016-195438
23	18	66.7	3001	4	US-09-539-333D-179
24	18	66.7	9098	4	US-09-358-082A-28
25	18	66.7	9098	4	US-09-358-082A-28
26	18	66.7	19296	4	US-09-949-016-16393
27	18	66.7	33731	4	US-09-949-016-13473

ALIGNMENTS

RESULT 1

US-09-949-016-12804
; Sequence 12804, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12804

; LENGTH: 64319

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-12804

Query Match 73.3%; Score 19.8; DB 4; Length 64319;

Best Local Similarity 91.3%; Pred. No. 80;

Matches 21; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 ATACATAACGAAACCTGAACA 24

Db 18750 ATAAATACAGAAACCTAAACA 18772

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RESULT 2

US-09-949-016-15906/c
; Sequence 15906, Application US/09949016
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CLO01307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

Sequence 13474, A
Sequence 13470, A
Sequence 13471, A
Sequence 15867, A
Sequence 16115, A
Sequence 12943, A
Sequence 13610, A
Sequence 14038, A
Sequence 12234, A
Sequence 3, Appli
Sequence 3, Appli
Sequence 12245, A
Sequence 12257, A
Sequence 13368, A
Sequence 17394, A
Sequence 17395, A
Sequence 16509, A
Sequence 3, Appli

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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 10:13:23 ; Search time 461.529 Seconds
(without alignments)
430.040 Million cell updates/sec

Title: US-10-025-137B-4

Perfect score: 24
Sequence: 1 acgcccgttaggtgattgtg 24

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 9794790 seqs, 4134909567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA.*

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26: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
27: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
28: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	24	100.0	24	US-10-025-137-4	Sequence 4, Appli
2	24	100.0	4402	US-10-450-763-25521	Sequence 25521, A
3	18	75.0	18	US-10-025-137-2	Sequence 2, Appli
4	17.2	71.7	225	US-10-724-972A-1325	Sequence 1325, Ap
5	17	70.8	25	US-10-719-900-455085	Sequence 455085,

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6 17 70.8 501 13 US-09-925-065A-816484 Sequence 816484,
7 16.8 70.0 611 13 US-09-925-065A-747394 Sequence 747394,
8 16.8 70.0 620 13 US-09-925-065A-735148 Sequence 735148,
9 16.8 70.0 1545 9 US-09-815-243-4756 Sequence 4756, Ap
10 16.8 70.0 1578 9 US-09-815-243-8828 Sequence 8828, Ap
11 16.8 70.0 1578 18 US-10-282-132A-7945 Sequence 7945, Ap
12 16.8 70.0 3730 24 US-10-795-159-481 Sequence 481, Appl
13 16.8 70.0 18355 8 US-08-781-986A-67 Sequence 67, Appl
14 16.8 70.0 18355 22 US-10-329-624-67 Sequence 67, Appl
15 16.8 70.0 28724 19 US-10-741-600-17808 Sequence 17808, A
16 16.8 70.0 36714 20 US-10-322-281-864 Sequence 864, App
17 16.8 70.0 60989 18 US-10-292-798-197 Sequence 197, App
18 16.8 70.0 417576 24 US-10-795-159-684 Sequence 684, App
19 16.8 70.0 1830121 18 US-10-329-670-1 Sequence 1, Appli
20 16.8 70.0 1830121 21 US-10-158-865-1 Sequence 1, Appli
21 16.8 70.0 1830121 24 US-10-981-687-1 Sequence 1, Appli
22 16.6 69.2 240 21 US-10-425-115-155871 Sequence 155871,
23 16.6 69.2 509 9 US-09-864-761-7520 Sequence 7520, Ap
24 16.6 69.2 509 17 US-10-029-386-3390 Sequence 3390, Ap
25 16.6 69.2 839 21 US-10-363-345A-15251 Sequence 15251, A
26 16.6 69.2 839 21 US-10-363-345A-15252 Sequence 15252, A
27 16.6 69.2 839 22 US-10-363-483A-15251 Sequence 15251, A
28 16.6 69.2 839 22 US-10-363-483A-15252 Sequence 15252, A
29 16.6 69.2 2724 24 US-10-450-763-10761 Sequence 10761, A
30 16.6 69.2 2729 24 US-10-450-763-21785 Sequence 21785, A
31 16.6 69.2 27681 9 US-09-764-869-1997 Sequence 1997, Ap
32 16.6 69.2 27681 9 US-09-764-869-1998 Sequence 1998, Ap
33 16.6 69.2 27681 15 US-10-091-504-1997 Sequence 1997, Ap
34 16.6 69.2 27681 15 US-10-091-504-1998 Sequence 1997, Ap
35 16.6 69.2 27681 18 US-10-227-577-1997 Sequence 1997, Ap
36 16.6 69.2 27681 18 US-10-227-577-1998 Sequence 1998, Ap
37 16.6 69.2 86114 16 US-10-080-170-648 Sequence 648, App
38 16.6 69.2 86114 20 US-10-080-170-648 Sequence 648, App
39 16.6 69.2 86114 20 US-10-468-356-648 Sequence 648, App
40 16.6 69.2 243390 20 US-10-322-281-462 Sequence 462, App
41 16.6 69.2 1830121 18 US-10-329-670-1 Sequence 1, Appli
42 16.6 69.2 1830121 21 US-10-158-865-1 Sequence 1, Appli
43 16.6 69.2 1830121 24 US-10-981-687-1 Sequence 1, Appli
44 16.6 68.3 583 13 US-09-925-065A-818153 Sequence 818153,
45 16.4 68.3 583 13 US-09-925-065A-841207 Sequence 841207,

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ALIGNMENTS

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RESULT 1
US-10-025-137-4
; Sequence 4, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Tserng, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025,137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated primer
US-10-025-137-4

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Query Match 100.0%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ACGCCGTAGGTGATTGTTG 24
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 06:12:54 ; Search time 62.3246 Seconds
(without alignments)
630.098 Million cell updates/sec

Title: US-10-025-137B-4
Perfect score: 24
Sequence: 1 acgcccgttaggtattgattgtg 24

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17.6	73.3	601	4	US-09-949-016-166018
2	17.6	73.3	234884	4	US-09-949-016-16420
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4	17.2	71.7	3005	4	US-09-710-279-3452
5	17.2	71.7	3065	4	US-09-710-279-3697
6	17.2	71.7	3172	4	US-09-710-279-3876
7	17.2	71.7	3172	4	US-09-710-279-4314
8	16.8	70.0	18355	4	US-08-956-171B-67
9	16.8	70.0	18355	4	US-08-781-986A-67
10	16.8	70.0	1830121	4	US-09-557-884-1
11	16.8	70.0	1830121	4	US-09-643-990A-1
12	16.6	69.2	227390	4	US-09-949-016-12201
13	16.6	69.2	227391	4	US-09-949-016-13365
14	16.6	69.2	1830121	4	US-09-557-884-1
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16	16.6	69.2	4403765	3	US-09-103-840A-2
17	16.6	69.2	4411529	3	US-09-103-840A-1
18	16.4	68.3	10783	4	US-09-949-016-16290
19	16.2	67.5	601	4	US-09-949-016-141180
20	16.2	67.5	2871	4	US-09-949-016-3998
21	16.2	67.5	3650	4	US-09-620-312B-30
22	16.2	67.5	29433	4	US-09-949-016-15740
23	16.2	67.5	1664976	4	US-08-916-421B-1
24	16.2	67.5	1664976	4	US-09-692-570-1
25	16	66.7	2613	3	US-09-221-017B-563
26	16	66.7	219944	4	US-09-949-016-15086
27	16	66.7	1664976	4	US-08-916-421B-1

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Sequence 272, App
Sequence 142400, A
Sequence 167522, A
Sequence 12014, A
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Sequence 15863, A
Sequence 15770, A
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Sequence 1135, Ap
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Sequence 1161, Ap
Sequence 4123, Ap
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15.8 65.8 58133 4 US-09-949-016-16464
15.8 65.8 96340 4 US-09-949-016-15863
15.8 65.8 211049 4 US-09-949-016-15770
15.6 65.0 390 4 US-09-489-039A-4446
15.6 65.0 501 4 US-09-489-039A-4446
15.6 65.0 526 4 US-08-956-171B-1135
15.6 65.0 526 4 US-08-781-986A-1135
15.6 756 4 US-09-134-000C-1161
15.6 65.0 1386 4 US-09-248-796A-4123
15.6 65.0 7278 3 US-09-091-219-1
15.6 65.0 7278 4 US-09-660-541-1
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ALIGNMENTS

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; Sequence 166018, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 166018
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-166018

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Best Local Similarity 83.3%; Pred. No. 46;
Matches 20; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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; Sequence 16420, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498

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OM nucleic - nucleic search, using sw model

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Title: US-10-025-137B-3

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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4	18.2	75.8	1224	26	US-11-097-143-31046
5	18.2	75.8	3224	26	US-11-097-143-31045

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Sequence 149388, A	700	18	US-10-027-632-149388	74.2	17.8	9	9
Sequence 47169, A	1221	18	US-10-369-493-47169	74.2	17.8	10	10
Sequence 842, App	1482	9	US-09-070-742A-842	74.2	17.8	11	11
Sequence 14, Appl	2658	9	US-09-027-927A-14	74.2	17.8	12	12
Sequence 14, Appl	2658	21	US-10-901-139-14	74.2	17.8	13	13
Sequence 310, App	550	14	US-10-663-561-310	73.3	17.6	14	14
Sequence 271125, A	554	20	US-10-027-632-271125	73.3	17.6	15	15
Sequence 271125, A	554	18	US-10-027-632-271125	73.3	17.6	16	16
Sequence 311952, A	581	13	US-09-925-065A-311952	73.3	17.6	17	17
Sequence 2910, Ap	919	9	US-09-815-242-2910	73.3	17.6	18	18
Sequence 5489, Ap	919	18	US-10-282-122A-5489	73.3	17.6	19	19
Sequence 22, Appl	972	19	US-10-109-310-22	73.3	17.6	20	20
Sequence 386, App	1006	8	US-08-781-986A-386	73.3	17.6	21	21
Sequence 386, App	1006	19	US-10-329-624-386	73.3	17.6	22	22
Sequence 23358, A	1170	20	US-10-437-963-23358	73.3	17.6	23	23
Sequence 674296, A	1260	13	US-09-925-065A-674296	73.3	17.6	24	24
Sequence 4375, Ap	1458	9	US-09-815-242-4375	73.3	17.6	25	25
Sequence 8209, Ap	1470	18	US-10-282-122A-8209	73.3	17.6	26	26
Sequence 423, App	1470	22	US-10-857-625-423	73.3	17.6	27	27
Sequence 8388, Ap	1515	9	US-09-815-242-8388	73.3	17.6	28	28
Sequence 50038, A	1515	20	US-10-437-963-50038	73.3	17.6	29	29
Sequence 260220, A	2238	14	US-10-027-632-260220	73.3	17.6	30	30
Sequence 260221, A	2238	14	US-10-027-632-260221	73.3	17.6	31	31
Sequence 260220, A	2238	18	US-10-027-632-260220	73.3	17.6	32	32
Sequence 260221, A	2238	18	US-10-027-632-260221	73.3	17.6	33	33
Sequence 121, App	2284	22	US-10-857-625-121	73.3	17.6	34	34
Sequence 3703, Ap	3641	18	US-10-398-221-3703	73.3	17.6	35	35
Sequence 41020, A	3641	26	US-11-097-143-41020	73.3	17.6	36	36
Sequence 32, Appl	3952	8	US-08-781-986A-32	73.3	17.6	37	37
Sequence 32, Appl	3952	19	US-10-329-624-32	73.3	17.6	38	38
Sequence 18, Appl	33000	19	US-10-109-310-18	73.3	17.6	39	39
Sequence 717, App	47804	16	US-10-017-161-717	73.3	17.6	40	40
Sequence 629, App	47804	18	US-10-292-798-629	73.3	17.6	41	41
Sequence 249, App	107304	20	US-10-322-281-249	73.3	17.6	42	42
Sequence 2, Appli	335913	10	US-09-754-853A-2	73.3	17.6	43	43
Sequence 3, Appli	335913	10	US-09-754-853A-3	73.3	17.6	44	44
Sequence 11, Appl	392000	16	US-10-027-983-11	73.3	17.6	45	45

ALIGNMENTS

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US-10-025-137-3
; Sequence 3, Application US/10025137
; Publication No. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Tering, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025,137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated primer
US-10-025-137-3

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Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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630.098 Million cell updates/sec

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	17.6	73.3	1006	4	US-08-956-171E-386
5	17.6	73.3	1006	4	US-08-781-986A-386
6	17.6	73.3	1101	4	US-09-328-352-1336
7	17.6	73.3	1888	3	US-08-737-226-3
8	17.6	73.3	2525	3	US-08-714-918-84
9	17.6	73.3	2525	3	US-09-265-115-84
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11	17.6	73.3	2525	3	US-09-266-417-84
12	17.6	73.3	2525	4	US-09-528-709-84
13	17.6	73.3	2525	4	US-09-527-745-84
14	17.6	73.3	10088	4	US-08-956-171E-32
15	17.6	73.3	10088	4	US-08-781-986A-32
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17	17.6	73.3	325034	4	US-09-949-016-114957
18	17.6	73.3	389504	4	US-09-949-016-11774
19	17.6	73.3	392000	4	US-10-027-983-11
20	17.2	71.7	163	4	US-09-513-999C-33278
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22	17.2	71.7	897	4	US-09-270-767-3490
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24	17.2	71.7	1908	4	US-09-543-681A-1784
25	17.2	71.7	11378	3	US-08-961-527-210
26	16.8	70.0	777	4	US-09-328-352-4023
27	16.8	70.0	142783	4	US-09-949-016-15127

28	16.8	70.0	818128	4	US-09-949-016-14546	Sequence 14546, A
29	16.8	70.0	818128	4	US-09-949-016-14547	Sequence 14547, A
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ALIGNMENTS

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; Patent No. 5891692
; GENERAL INFORMATION:
; APPLICANT: BLOOM, FREDERIC
; APPLICANT: KUO, JONATHAN
; APPLICANT: LIN, JHY-JHU
; APPLICANT: MA, JIN
; TITLE OF INVENTION: METHOD FOR INCREASING VIABILITY
; TITLE OF INVENTION: AND TRANSFORMATION EFFICIENCY OF BACTERIA DURING
; TITLE OF INVENTION: STORAGE AT LOW TEMPERATURES
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20004-2402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
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; FILING DATE: 27-MAR-1997
; CLASSIFICATION: 435
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; APPLICATION NUMBER: U.S. Ser. No. 5891692 60/014,330
; FILING DATE: 29-MAR-1996
; APPLICATION NUMBER: U.S. Ser. No. 5891692 60/025,838
; FILING DATE: 05-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Auerbach, Jeffrey
; REGISTRATION NUMBER: 32,680
; REFERENCE/DOCKET NUMBER: 04227-0031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202 383-7451
; TELEFAX: 202 383-6610
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2658 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-826-426-14

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OM nucleic - nucleic search, using sw model

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	16	US-10-025-137-2
2	18	100.0	24	16	Sequence 2, Appli
3	18	100.0	4402	24	US-10-025-137-4
4	16.4	91.1	1060	10	US-10-450-763-25521
5	16	88.9	501	13	US-09-764-872-808
					Sequence 808, App
					Sequence 816484,

c 6	15.4	85.6	497	13	US-09-925-065A-182186	Sequence 182186,
c 7	15.4	85.6	497	13	US-09-925-065A-182187	Sequence 182187,
c 8	15.4	85.6	522	17	US-10-029-386-5126	Sequence 5126, Ap
c 9	15.4	85.6	537	14	US-10-027-632-186868	Sequence 186868,
c 10	15.4	85.6	537	18	US-10-027-632-186868	Sequence 186868,
c 11	15.4	85.6	534	13	US-09-925-065A-406303	Sequence 406303,
c 12	15.4	85.6	572	14	US-10-027-632-225990	Sequence 225990,
c 13	15.4	85.6	572	18	US-10-027-632-225990	Sequence 225990,
c 14	15.4	85.6	583	13	US-09-925-065A-818153	Sequence 818153,
c 15	15.4	85.6	583	13	US-09-925-065A-841207	Sequence 841207,
c 16	15.4	85.6	604	14	US-10-027-632-212524	Sequence 212524,
c 17	15.4	85.6	604	18	US-10-027-632-212524	Sequence 212524,
c 18	15.4	85.6	611	13	US-09-925-065A-747394	Sequence 747394,
c 19	15.4	85.6	618	13	US-09-925-065A-246000	Sequence 246000,
c 20	15.4	85.6	620	13	US-09-925-065A-735148	Sequence 735148,
c 21	15.4	85.6	656	13	US-09-925-065A-415746	Sequence 415746,
c 22	15.4	85.6	820	14	US-10-027-632-173633	Sequence 173633,
c 23	15.4	85.6	820	14	US-10-027-632-173634	Sequence 173634,
c 24	15.4	85.6	820	18	US-10-027-632-173633	Sequence 173633,
c 25	15.4	85.6	820	18	US-10-027-632-173634	Sequence 173634,
c 26	15.4	85.6	1214	14	US-10-027-632-212523	Sequence 212523,
c 27	15.4	85.6	1214	18	US-10-027-632-212523	Sequence 212523,
c 28	15.4	85.6	1545	9	US-09-815-242-4756	Sequence 4756, Ap
c 29	15.4	85.6	1578	9	US-09-815-242-8828	Sequence 8828, Ap
c 30	15.4	85.6	1578	18	US-10-282-122A-7945	Sequence 7945, Ap
c 31	15.4	85.6	3129	18	US-10-282-122A-11102	Sequence 11102, A
c 32	15.4	85.6	3540	18	US-10-282-122A-24459	Sequence 24459, A
c 33	15.4	85.6	4053	9	US-09-070-927A-407	Sequence 407, App
c 34	15.4	85.6	5185	16	US-10-311-455-1008	Sequence 1008, Ap
c 35	15.4	85.6	5518	16	US-10-240-453-180	Sequence 180, App
c 36	15.4	85.6	6624	16	US-10-311-455-16	Sequence 16, Appl
c 37	15.4	85.6	7168	19	US-10-240-589C-39	Sequence 39, Appl
c 38	15.4	85.6	12138	16	US-10-311-455-1601	Sequence 1601, Ap
c 39	15.4	85.6	12138	18	US-10-257-166-115	Sequence 115, App
c 40	15.4	85.6	17280	19	US-10-221-714A-497	Sequence 497, App
c 41	15.4	85.6	18355	8	US-08-781-986A-67	Sequence 67, Appl
c 42	15.4	85.6	61020	19	US-10-329-624-67	Sequence 67, Appl
c 43	15.4	85.6	61020	19	US-10-221-714A-514	Sequence 514, App
c 44	15	83.3	465	14	US-10-027-632-83432	Sequence 83432, A
c 45	15	83.3	465	14	US-10-027-632-83433	Sequence 83433, A

ALIGNMENTS

RESULT 1
US-10-025-137-2
; Sequence 2, Application US/10025137
; Publication NO. US20030113731A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Lu-Yieng
; APPLICANT: Chung, Te-Yu
; APPLICANT: Tsering, Harn-Jing
; TITLE OF INVENTION: METHOD FOR DETECTING ESCHERICHIA COLI
; FILE REFERENCE: 12674-005001
; CURRENT APPLICATION NUMBER: US/10/025,137
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetically generated primer
US-10-025-137-2

Query Match 100.0%; Score 18; DB 16; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TTAGGTGATTGTTGTTG 18
|||||||

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 4, 2005, 06:12:54 ; Search time 46.7435 Seconds
(without alignments)
630.098 Million cell updates/sec

Title: US-10-025-137B-2

Perfect score: 18
Sequence: 1 ttagggtattgattgtg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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3: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16.4	91.1	10783	4	US-09-949-016-16290 Sequence 16290, A
2	15.4	85.6	309	4	US-09-134-000C-272 Sequence 272, App
3	15.4	85.6	1386	4	US-09-248-796A-4123 Sequence 4123, Ap
C 4	15.4	85.6	1800	4	US-09-248-796A-4214 Sequence 4214, Ap
C 5	15.4	85.6	18355	4	US-08-956-171E-67 Sequence 67, Appl
C 6	15.4	85.6	18355	4	US-08-781-986A-67 Sequence 67, Appl
C 7	15	83.3	1596	3	US-09-134-001C-737 Sequence 737, App
8	15	83.3	236341	4	US-09-949-016-13978 Sequence 13978, A
9	14.8	82.2	390	4	US-09-489-039A-4446 Sequence 4446, Ap
C 10	14.8	82.2	457	4	US-09-621-976-130 Sequence 130, App
C 11	14.8	82.2	496	3	US-09-036-574-6 Sequence 6, Appli
C 12	14.8	82.2	496	4	US-08-454-294A-6 Sequence 467, Ap
C 13	14.8	82.2	501	4	US-09-489-039A-4467 Sequence 4467, Ap
C 14	14.8	82.2	601	4	US-09-949-016-142400 Sequence 142400, Sequence 166018,
C 15	14.8	82.2	601	4	US-09-949-016-166018 Sequence 166018,
C 16	14.8	82.2	601	4	US-09-949-016-167522 Sequence 167522,
C 17	14.8	82.2	1132	3	US-09-036-574-8 Sequence 8, Appli
C 18	14.8	82.2	1132	4	US-08-454-294A-8 Sequence 151, App
C 19	14.8	82.2	1137	4	US-09-248-796A-151 Sequence 3, Appli
C 20	14.8	82.2	1703	4	US-09-057-996-3 Sequence 200, App
C 21	14.8	82.2	6091	3	US-09-453-702B-200 Sequence 12868, A
C 22	14.8	82.2	15402	4	US-09-949-016-12868 Sequence 13826, A
C 23	14.8	82.2	17842	4	US-09-949-016-13826 Sequence 13826, A
C 24	14.8	82.2	24000	4	US-09-949-016-14421 Sequence 14421, A
C 25	14.8	82.2	39433	4	US-09-949-016-12014 Sequence 12014, A
C 26	14.8	82.2	42075	4	US-09-949-016-14995 Sequence 14995, A
C 27	14.8	82.2	58133	4	US-09-949-016-16464 Sequence 16464, A

28	14.8	82.2	88906	4	US-09-949-016-17468 Sequence 17468, A
29	14.8	82.2	96340	4	US-09-949-016-15863 Sequence 15863, A
30	14.8	82.2	139552	4	US-09-949-016-15300 Sequence 15300, A
31	14.8	82.2	211049	4	US-09-949-016-15770 Sequence 15770, A
32	14.8	82.2	234884	4	US-09-949-016-16420 Sequence 16420, A
33	14.8	82.2	253345	4	US-09-949-016-12656 Sequence 12656, A
34	14.8	82.2	253364	4	US-09-949-016-13639 Sequence 13639, A
35	14.8	82.2	340380	4	US-09-949-016-14179 Sequence 14179, A
36	14.8	82.2	1664976	4	US-08-916-421B-1 Sequence 1, Appli
37	14.8	82.2	1664976	4	US-09-692-570-1 Sequence 1, Appli
38	14.4	80.0	204	4	US-09-248-796A-7582 Sequence 7582, Ap
C 39	14.4	80.0	234	4	US-09-495-050A-121 Sequence 121, App
C 40	14.4	80.0	360	4	US-09-248-796A-7584 Sequence 7584, Ap
41	14.4	80.0	543	4	US-09-134-000C-2288 Sequence 2288, Ap
42	14.4	80.0	603	4	US-09-540-236-607 Sequence 607, App
C 43	14.4	80.0	1101	4	US-09-543-681A-3334 Sequence 3334, Ap
44	14.4	80.0	1347	4	US-09-134-000C-479 Sequence 479, App
45	14.4	80.0	3282	4	US-09-511-881A-12 Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-16290
; Sequence 16290, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 16290
; LENGTH: 10783
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-16290

Query Match 91.1% Score 16.4; DB 4; Length 10783;
Best Local Similarity 94.4% Pred. No. 90;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 4089 TTAGGTGATTGATTGTG 4106

RESULT 2
US-09-134-000C-272
; Sequence 272, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 272